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Guy Beardsley

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Rima Rozen

Art Unit: Not Yet Assigned

Serial No.: Not Yet Assigned

Examiner: Not Yet Assigned

Filed: August 16, 2001

Customer No.: 21559

Title: cDNA FOR HUMAN METHYLENETETRAHYDROFOLATE  
REDUCTASE AND USES THEREOF

Assistant Commissioner For Patents  
Washington, D.C. 20231

PRELIMINARY AMENDMENT

Prior to examination of the above-referenced application, kindly consider the following amendments and remarks.

In the Claims:

Cancel claims 1-28 and 53-69, without prejudice.

In the Specification:

Please replace the first paragraph of the specification with the following paragraph that has been re-written in clean form.

This application is a divisional of pending US patent application serial number 09/592,595 filed June 12, 2000, which is a continuation-in-part of US patent application serial number 09/258,928 filed March 1, 1999 (now US patent number 6,218,120), which is a continuation in part of US patent application serial number 08/738,000 filed February 12, 1997 (now US patent number 6,074,821), which claims priority from PCT CA 95/00314, filed May 25, 1995, and GB 9410620.0, filed May 26, 1994.

Please replace the paragraph on page 60, line 8, through page 61, line 9, of the specification with the following paragraph that has been re-written in clean form.

Patients with spina bifida and mothers of patients were recruited from the Spina Bifida Clinic at the Montreal Children's Hospital following approval from the Institutional Review Board. Control children and mothers of controls were recruited from the same institution. Blood samples were used to prepare DNA from peripheral leukocytes, to assay MTHFR activity in lymphocyte extracts, and to measure total plasma homocysteine (tHcy). The presence of the C677T mutation (A to V) was evaluated by PCR and HinfI digestion (2). The A1298C mutation was initially examined by PCR and MboII digestion (5). The silent mutation, T1317C, was identified by SSCP and sequence analysis in a patient with severe MTHFR deficiency and homocystinuria. This patient, an African-American female, already carries a previously-described splice mutation (patient 354 (8)). Since this mutation also creates a MboII site and results in a digestion pattern identical to that of the A1298C mutation, distinct artificially-created restriction sites were used to distinguish between these 2 mutations. Detection of the A1298C polymorphism was performed with the use of the sense primer 5'-GGGAGGAGCTGACCAGTGCAG-3' (SEQ ID NO:15) and the antisense primer (5'-GGGGTCAGGCCAGGGGCAG-3', SEQ ID NO:16), such that the 138bp PCR fragment was digested into 119bp and 19bp fragments by Fnu4HI in the presence of the C allele. An antisense primer (5'-GGTTCTCCCGAGAGGTAAAGATC-3', SEQ ID NO:17), which introduces a TaqI site, was similarly designed to identify the C allele of the T1317C polymorphism. Together with a sense primer (5'-CTGGGGATGTGGTGGCACTGC-3', SEQ ID NO:18), the 227bp fragment is digested into 202bp and 25bp fragments.

Kindly insert the enclosed sequence listing at the end of the application.

## REMARKS

The specification has been amended to provide a unique sequence identification number for each nucleotide sequence within the specification. The attached sequence listing has also been inserted into the application. No new matter is introduced by any of the amendments.

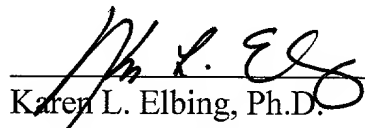
## CONCLUSION

Applicants submit that this application is now in condition for allowance, and such action is respectfully requested. A marked-up version indicating the amendments made to the specification, as required by 37 C.F.R. § 1.121(b)(1)(iii), is enclosed.

If there are any charges, or any credits, please apply them to Deposit Account No. 03-2095.

Respectfully submitted,

Date: 16 August 2001

  
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F:\04844\04844.005005 Preliminary amendment wpd



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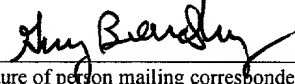
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Version with Markings to Show Changes Made

A marked-up version of the first paragraph of the specification is presented below.

"This application is a divisional of pending US patent application serial number 09/592,595 filed June 12, 2000, which is a continuation-in-part of US patent application serial number 09/258,928 filed March 1, 1999 (now US patent number 6,218,120), which is a continuation in part of US patent application serial number 08/738,000 filed February 12, 1997 (now US patent number 6,074,821), which claims priority from PCT CA 95/00314, filed May 25, 1995, and GB 9410620.0, filed May 26, 1994."

A marked-up version of the paragraph on page 60, line 8, through page 61, line 9, of the specification is presented below.

“Patients with spina bifida and mothers of patients were recruited from the Spina Bifida Clinic at the Montreal Children's Hospital following approval from the Institutional Review Board. Control children and mothers of controls were recruited from the same institution. Blood samples were used to prepare DNA from peripheral leukocytes, to assay MTHFR activity in lymphocyte extracts, and to measure total plasma homocysteine (tHcy). The presence of the C677T mutation (A to V) was evaluated by PCR and *Hinf*I digestion (2). The A1298C mutation was initially examined by PCR and *Mbo*II digestion (5). The silent mutation, T1317C, was identified by SSCP and sequence analysis in a patient with severe MTHFR deficiency and homocystinuria. This patient, an African-American female, already carries a previously-described splice mutation (patient 354 (8)). Since this mutation also creates a *Mbo*II site and results in a digestion pattern identical to that of the A1298C mutation, distinct artificially-created restriction sites were used to distinguish between these 2 mutations. Detection of the A1298C polymorphism was performed with the use of the sense primer 5'-GGGAGGAGCTGACCAGTGCAG-3' (SEQ ID NO:15) and the antisense primer (5'-GGGGTCAGGCCAGGGGCAG-3', SEQ ID NO:16), such that the 138bp PCR fragment was digested into 119bp and 19bp fragments by *Fnu*4HI in the presence of the C allele. An antisense primer (5'-GGTTCTCCCGAGAGGTAAAGATC-3', SEQ ID NO:17), which introduces a *Taq*I site, was similarly designed to identify the C allele of the T1317C polymorphism. Together with a sense primer (5'-CTGGGGATGTGGTGGCACTGC-3', SEQ ID NO:18), the 227bp fragment is digested into 202bp and 25bp fragments.”

04844.005005 Preliminary amendment.wpd